L3 ANSWER 26 OF 64 CAPLUS COPYRIGHT 2005 ACS on STN
ACCESSION NUMBER: 1999:218801 CAPLUS
DOCUMENT NUMBER: 131:29241
TITLE: DNA demethylase is a processive enzyme
AUTHOR(S): Cervoni, Nadia; Bhattacharya, Sanjoy; **Szyf, Moshe**
CORPORATE SOURCE: Department of Pharmacology, McGill University, Montreal, QC, H3G 1Y6, Can.
SOURCE: Journal of Biological Chemistry (**1999**), 274(13), 8363-8366
CODEN: JBCHA3; ISSN: 0021-9258
PUBLISHER: American Society for Biochemistry and Molecular Biology
DOCUMENT TYPE: Journal
LANGUAGE: English
ABSTRACT:
DNA methylation patterns are generated during development by a sequence of methylation and demethylation events. We have recently demonstrated that mammals bear a bona fide demethylase enzyme that removes Me groups from methylated cytosines. A general genome wide demethylation occurs early in development and in differentiating cell lines. This manuscript tests the hypothesis that the demethylase enzyme is a processive enzyme. Using bisulfite mapping, this report demonstrates that demethylase is a processive enzyme and that the rate-limiting step in demethylation is the initiation of demethylation. Initiation of demethylation is determined by the properties of the sequence. Once initiated, demethylation progresses processively. We suggest that these data provide a mol. explanation for global hypomethylation.

REFERENCE COUNT: 20 THERE ARE 20 CITED REFERENCES AVAILABLE FOR THIS RECORD. ALL CITATIONS AVAILABLE IN THE RE FORMAT

L3 ANSWER 28 OF 64 CAPLUS COPYRIGHT 2005 ACS on STN

ACCESSION NUMBER: 1999:137598 CAPLUS
DOCUMENT NUMBER: 130:308265
TITLE: A mammalian protein with specific demethylase activity for mCpG DNA
AUTHOR(S): Bhattacharya, Sanjoy K.; Ramchandani, Shyam; Cervoni, Nadia; **Szyf, Moshe**
CORPORATE SOURCE: Department of Pharmacology and Therapeutics, McGill University, Montreal, QC, H3G 1Y6, Can.
SOURCE: Nature (London) (**1999**), 397(6720), 579-583
CODEN: NATUAS; ISSN: 0028-0836
PUBLISHER: Macmillan Magazines
DOCUMENT TYPE: Journal
LANGUAGE: English
ABSTRACT:

DNA-methylation patterns are important for regulating genome functions, and are determined by the enzymic processes of methylation and demethylation. The demethylating enzyme has now been identified: a mammalian complementary DNA encodes a methyl-CpG-binding domain, bears a demethylase activity that transforms methylated cytosine bases to cytosine, and demethylates a plasmid when the cDNA is translated or transiently transfected into human embryonal kidney cells in vitro. The discovery of this DNA demethylase should provide a basis for the mol. and developmental anal. of the role of DNA methylation and demethylation.

REFERENCE COUNT: 28 THERE ARE 28 CITED REFERENCES AVAILABLE FOR THIS RECORD. ALL CITATIONS AVAILABLE IN THE RE FORMAT

L3 ANSWER 29 OF 64 CAPLUS COPYRIGHT 2005 ACS on STN
ACCESSION NUMBER: 1998:795124 CAPLUS
DOCUMENT NUMBER: 130:48320
TITLE: Human DNA methyltransferase genomic sequences and antisense oligonucleotides
INVENTOR(S): **Szyf, Moshe**; Bigey, Pascal; Ramchandani, Shyam
PATENT ASSIGNEE(S): McGill University, Can.
SOURCE: PCT Int. Appl., 108 pp.
CODEN: PIXXD2
DOCUMENT TYPE: Patent
LANGUAGE: English
FAMILY ACC. NUM. COUNT: 1
PATENT INFORMATION:

PATENT NO.	KIND	DATE	APPLICATION NO.	DATE
WO 9854313	A2	19981203	WO 1998-IB1107	19980529 <--
WO 9854313	A3	19990401		
W: AL, AM, AT, AU, AZ, BA, BB, BG, BR, BY, CA, CH, CN, CU, CZ, DE, DK, EE, ES, FI, GB, GE, GH, GM, GW, HU, ID, IL, IS, JP, KE, KG, KP, KR, KZ, LC, LK, LR, LS, LT, LU, LV, MD, MG, MK, MN, MW, MX, NO, NZ, PL, PT, RO, RU, SD, SE, SG, SI, SK, SL, TJ, TM, TR, TT, UA, UG, UZ, VN, YU, ZW, AM, AZ, BY, KG, KZ, MD, RU, TJ, TM				
RW: GH, GM, KE, LS, MW, SD, SZ, UG, ZW, AT, BE, CH, CY, DE, DK, ES, FI, FR, GB, GR, IE, IT, LU, MC, NL, PT, SE, BF, BJ, CF, CG, CI, CM, GA, GN, ML, MR, NE, SN, TD, TG				
US 6020318	A	20000201	US 1997-866340	19970530 <--
CA 2291595	AA	19981203	CA 1998-2291595	19980529 <--
AU 9881250	A1	19981230	AU 1998-81250	19980529 <--
EP 985035	A2	20000315	EP 1998-930981	19980529 <--
R: AT, BE, CH, DE, DK, ES, FR, GB, GR, IT, LI, LU, NL, SE, MC, PT, IE, FI				
JP 2002512508	T2	20020423	JP 1998-536061	19980529
US 6221849	B1	20010424	US 1998-103875	19980624 <--

PRIORITY APPLN. INFO.:		
US 1997-866340	A	19970530
US 1997-69865P	P	19971217
WO 1998-IB1107	W	19980529

ABSTRACT:
The invention provides recombinant nucleic acids comprising nucleic acid sequences from the genomic DNA methyltransferase gene. The invention further provides sequence information for such nucleic acid sequences. The human gene is organized as 40 exons and 39 introns, with completely conserved splice acceptor and donor sites, on 60 kb of chromosome 19p13.2-13.3. Thus, the gene offers 78 unique intron-exon junctions for antisense oligonucleotide design. In addition, the invention provides 32 antisense oligonucleotides complementary to special regions of the genomic DNA methyltransferase gene or its RNA transcript. Specific antisense oligonucleotides are shown to inhibit expression of DNA methyltransferase as well as to inhibit tumor growth inhibition. Methods for using such antisense oligonucleotides as anal. and diagnostic tools, as potentiators of transgenic plant and animal studies and gene therapy approaches, and as potential therapeutic agents are provided.